

SEQUENCE LISTING

<110> Ruben et al.

<120> Cytokine Receptor Common Gamma Chain Like

<130> PF466P2

<150> 60/269,876

<151> 2001-02-21

<150> PCT/US00/22493

<151> 2000-08-17

<150> 09/376,430

<151> 1999-08-18

<150> 09/263,626

<151> 1999-03-05

<150> PCT/US99/05068

<151> 1999-03-05

<150> 60/086,505

<151> 1998-05-22

<150> 60/078,563

<151> 1998-03-19

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 1573

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(1125)

<400> 1

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ctg ctg gga ggc tgg atg gct ttg ggg caa gga gga gca gca gaa gga 99
Leu Leu Gly Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly
    15                      20                      25

gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca 147
Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr
    30                      35                      40                      45

tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga 195
Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg
      50                      55                      60

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ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag	243
Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln	
65 70 75	
gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac	291
Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp	
80 85 90	
att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca	339
Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala	
95 100 105	
agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg	387
Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val	
110 115 120 125	
aga ttt tcg tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg	435
Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu	
130 135 140	
tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac	483
Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp	
145 150 155	
acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa	531
Thr Glu Trp Gln Ser Lys Gln Asn Thr Cys Asn Val Thr Ile Glu	
160 165 170	
ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct	579
Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala	
175 180 185	
atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag	627
Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu	
190 195 200 205	
gtg aca tgc tgg cag aga ggc gag att cgg gat gcc tgt gca gag aca	675
Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr	
210 215 220	
cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc	723
Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser	
225 230 235	
ctg gcc atc ctt ctg atg gtg tct ctc ctc ctt ctg tct tta tgg aaa	771
Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Ser Leu Trp Lys	
240 245 250	
tta tgg aga gtg aag aag ttt ctc att ccc agc gtg cca gac ccg aaa	819
Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys	
255 260 265	
tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag	867
Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu	
270 275 280 285	
tgg atc aca gac acc'cag aac gtg gcc cac ctc cac aag atg gca ggt	915
Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly	
290 295 300	

gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc 963
 Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala
 305 310 315

aag act gaa gcc gag tct ccc agg atg ctg gac cca cag acc gag gag 1011
 Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu
 320 325 330

aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa 1059
 Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln
 335 340 345

ggc ggt gat gtg gtc aca atc ggg ggc ttc acc ttt gtg atg aat gac 1107
 Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp
 350 355 360 365

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 Arg Ser Tyr Val Ala Leu
 370

caggatccac gttgacattt aaagacagag gggactgtcc cggggactcc acaccaccat 1215

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 <213> Homo sapiens

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 20 25 30

Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala
 35 40 45

Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly
 50 55 60

Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His
 65 70 75 80

Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr
 85 90 95

Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp
100 105 110

Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser
115 120 125

Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly
130 135 140

Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp
145 150 155 160

Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp
165 170 175

Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp
180 185 190

Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys
195 200 205

Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro
210 215 220

Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile
225 230 235 240

Leu Leu Met Val Ser Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg
245 250 255

Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe
260 265 270

Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr
275 280 285

Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln
290 295 300

Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu
305 310 315 320

Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala
325 330 335

Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp
340 345 350

Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp Arg Ser Tyr
355 360 365

Val Ala Leu
370

<210> 3
<211> 379

<212> PRT

<213> Homo sapiens

<400> 3

Met Leu Lys Pro Pro Leu Pro Leu Arg Ser Leu Leu Phe Leu Gln Leu
1 5 10 15

Pro Leu Leu Gly Val Gly Leu Asn Pro Lys Phe Leu Thr Pro Ser Gly
20 25 30

Asn Glu Asp Ile Gly Gly Lys Pro Gly Thr Gly Gly Asp Phe Phe Leu
35 40 45

Thr Ser Thr Pro Ala Gly Thr Leu Asp Val Ser Thr Leu Pro Leu Pro
50 55 60

Lys Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met Asn Cys Thr Trp
65 70 75 80

Asn Ser Ser Ser Glu Pro Gln Pro Asn Asn Leu Thr Leu His Tyr Gly
85 90 95

Tyr Arg Asn Phe Asn Gly Asp Asp Lys Leu Gln Glu Cys Gly His Tyr
100 105 110

Leu Phe Ser Glu Gly Ile Thr Ser Gly Cys Trp Phe Gly Lys Lys Glu
115 120 125

Ile Arg Leu Tyr Glu Thr Phe Val Val Gln Leu Gln Asp Pro Arg Glu
130 135 140

His Arg Lys Gln Pro Lys Gln Met Leu Lys Leu Gln Asp Leu Val Ile
145 150 155 160

Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg Asn Leu Ser Glu Phe Gln
165 170 175

Leu Glu Leu Ser Trp Ser Asn Arg Tyr Leu Asp His Cys Leu Glu His
180 185 190

Leu Val Gln Tyr Arg Ser Asp Arg Asp Arg Ser Trp Thr Glu Gln Ser
195 200 205

Val Asp His Arg His Ser Phe Ser Leu Pro Ser Val Asp Ala Gln Lys
210 215 220

Leu Tyr Thr Phe Arg Val Arg Ser Arg Tyr Asn Pro Leu Cys Gly Ser
225 230 235 240

Ala Gln His Trp Ser Asp Trp Ser Tyr Pro Ile His Trp Gly Ser Asn
245 250 255

Thr Ser Lys Glu Asn Ile Glu Asn Pro Glu Asn Pro Ser Leu Phe Ala
260 265 270

Leu Glu Ala Val Leu Ile Pro Leu Gly Ser Met Gly Leu Ile Val Ser
275 280 285

Leu Ile Cys Val Tyr Cys Trp Leu Glu Arg Thr Met Pro Arg Ile Pro

290 295 300

Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr Gln Gly Asn Phe
305 310 315 320

Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro
325 330 335

Asp Tyr Ser Glu Arg Leu Cys His Val Ser Glu Ile Pro Pro Lys Gly
340 345 350

Gly Glu Gly Pro Gly Gly Ser Pro Cys Ser Gln His Ser Pro Tyr Trp
355 360 365

Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Pro
370 375

<210> 4
<211> 733
<212> DNA
<213> Homo sapiens

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tcctccggag tcctgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagcccgagg 240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360
agaaaaccat ctccaaagcc aaaggggcag cccgagaacc acaggtgtac accctgcccc 420
catcccgagg tgagctgacc aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct 480
atccaaagca catcgccgtg gagtgggaga gcaatgggca gccggagaa aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct ccttcttct ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag gggaaagctc tctcatgtct cgtgatgcat gaggctctgc 660
acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
gactctagag gat 733

<210> 5
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any amino acid

<400> 5
Trp Ser Xaa Trp Ser
1 5

<210> 6
<211> 86
<212> DNA
<213> Artificial Sequence

<220>
 <221> Primer_Bind
 <223> Synthetic sequence with 4 tandem copies of the GAS binding site found in the IRF1 promoter (Rothman et al., Immunity 1:457-468 (1994)), 18 nucleotides complementary to the SV40 early promoter, and a Xho I restriction site.

<400> 6
 gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aaatgatttc 60
 cccgaaatat ctgccatctc aattag 86

<210> 7
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Primer_Bind
 <223> Synthetic sequence complementary to the SV40 promoter; includes a Hind III restriction site.

<400> 7
 gcggcaagct ttttgcaaag cctaggc 27

<210> 8
 <211> 271
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Protein_Bind
 <223> Synthetic promoter for use in biological assays; includes GAS binding sites found in the IRF1 promoter (Rothman et al., Immunity 1:457-468 (1994)).

<400> 8
 ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60
 aaatatctgc catctcaatt agtcagcaac catagtcccc cccctaactc cgccccatccc 120
 gccctcaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
 ttatgcagag gccgaggccg cctcggcctc tgagctatcc cagaagtagt gaggaggcctt 240
 ttttgagggc ctaggctttt gcaaaaagct t 271

<210> 9
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Primer_Bind
 <223> Synthetic primer complementary to human genomic EGR-1 promoter sequence (Sakamoto et al., Oncogene 6:867-871 (1991)); including an Xho I restriction site.

<400> 9
 gcgcctcgagg gatgacagcg atagaacccc gg 32

<210> 10
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Primer_Bind
 <223> Synthetic primer complementary to human genomic EGR-1 promoter
 sequence (Sakamoto et al., Oncogene 6:867-871 (1991)); including an
 Hind III restriction site.

 <400> 10
 gcgaagcttc gcgactcccc ggatccgcct c 31

 <210> 11
 <211> 12
 <212> DNA
 <213> Homo sapiens

 <400> 11
 ggggactttc cc 12

 <210> 12
 <211> 73
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Primer_Bind
 <223> Synthetic primer with 4 tandem copies of the NF-KB binding
 site (GGGGACTTTCCC), 18 nucleotides complementary to the 5' end
 of the SV40 early promoter sequence, and a XhoI restriction site.

 <400> 12
 gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatctcg 60
 ccattcctcaat tag 73

 <210> 13
 <211> 256
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Protein_Bind
 <223> Synthetic promoter for use in biological assays; including
 NF-KB binding sites.

 <400> 13
 ctcgagggga ctttccccgg gactttccgg ggactttccg ggactttcca tctgccatct 60
 caattagtca gcaaccatag tccccccct aactccgcc atcccccccc taactccgcc 120
 cagttccgcc cattctccgc cccatggctg actaattttt ttattttatg cagaggccga 180
 ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240
 cttttgcaaa aagctt 256

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Primer_Bind
 <223> Synthetic primer containing the Nco I restriction site
 followed a number of nucleotides of the amino terminal coding
 sequence of CRCGCL

 <400> 14
 gttaggccat gggaggagca gcagaagga 29

 <210> 15
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Primer_Bind
 <223> Synthetic primer containing the BglII restriction site
 followed by a number nucleotides complementary to the 3' end
 of the coding sequence of CRCGCL

 <400> 15
 ggttaaagat ctcaacgccca cgtaggagcg gtc 33

 <210> 16
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Primer_Bind
 <223> Synthetic primer to amplify the cDNA sequence encoding the
 full length CRCGCL protein including the AUG initiation codon and
 the naturally associated leader,also contains a BglII site,and
 Kozak signal

 <400> 16
 ccggttagat ctgccatcat ggctttgggg caaggagg 38

 <210> 17
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> Primer_Bind
 <223> Synthetic primercontaining the XbaI restriction site followed
 by a number of nucleotides complementary to the 3' noncoding sequence
 of SEQ ID NO:1

 <400> 17
 ccggtttcta gatcacaagg ccacgtagga gcggtc 36

<210> 18
 <211> 7
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SITE
 <222> (1)
 <223> Xaa equals Ser, Thr, Gly or Leu

<220>
 <221> SITE
 <222> (2)
 <223> Xaa equals any amino acid

<220>
 <221> SITE
 <222> (4)
 <223> Xaa equals Ser or Gly

<220>
 <221> SITE
 <222> (5)
 <223> Xaa equals any amino acid

<400> 18
 Xaa Xaa Trp Xaa Xaa Trp Ser
 1 5

<210> 19
 <211> 7
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (2)
 <223> Xaa equals any amino acid

<220>
 <221> SITE
 <222> (5)
 <223> Xaa equals any amino acid

<400> 19
 Thr Xaa Pro Ser Xaa Trp Ser
 1 5

<210> 20
 <211> 7
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE

<222> (2)
 <223> Xaa equals Pro or Glu

 <220>
 <221> SITE
 <222> (3)
 <223> Xaa equals any amino acid

 <220>
 <221> SITE
 <222> (4)
 <223> Xaa equals Val or Ile

 <220>
 <221> SITE
 <222> (6)
 <223> Xaa equals Asn, Ser or Asp

<400> 20
 Trp Xaa Xaa Xaa Pro Xaa Pro
 1 5

<210> 21
 <211> 7
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (3)
 <223> Xaa equals any amino acid

<400> 21
 Ile Pro Xaa Val Pro Asp Pro
 1 5

<210> 22
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 22
 Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp
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Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe
 20 25 30

Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu
 35 40 45

Gly His Thr Ser Gly Cys
 50

<210> 23
 <211> 30

<212> PRT
<213> Homo sapiens

<400> 23
Arg Arg His Ser Leu Phe Leu His Gln Glu Trp Asp Ala Pro Arg Phe
1 5 10 15

His Arg Lys Ser Leu Asp Gly Leu Leu Pro Glu Thr Gln Phe
20 25 30

<210> 24
<211> 81
<212> PRT
<213> Homo sapiens

<400> 24
Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp Gln
1 5 10 15

Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp Ala
20 25 30

Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp Val
35 40 45

Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys Trp
50 55 60

Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro Pro
65 70 75 80

Lys

<210> 25
<211> 181
<212> PRT
<213> Homo sapiens

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<222> (68)
<223> Xaa equals any amino acid

<220>
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<222> (73)
<223> Xaa equals any amino acid

<220>
<221> SITE
<222> (88)
<223> Xaa equals any amino acid

<400> 25
Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu
1 5 10 15

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 20 25 30
 Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser
 35 40 45
 Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Ser Leu Trp Lys
 50 55 60
 Leu Trp Arg Xaa Lys Lys Phe Leu Xaa Pro Ser Val Pro Asp Pro Lys
 65 70 75 80
 Ser Ile Phe Pro Gly Leu Phe Xaa Ile His Gln Gly Asn Phe Gln Glu
 85 90 95
 Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly
 100 105 110
 Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala
 115 120 125
 Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu
 130 135 140
 Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln
 145 150 155 160
 Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp
 165 170 175
 Arg Ser Tyr Val Ala
 180

<210> 26
 <211> 1567
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (830)
 <223> n equals a, t, g or c

 <220>
 <221> misc_feature
 <222> (416)
 <223> y equals c or t

 <220>
 <221> misc_feature
 <222> (784)
 <223> m equals a or c

 <220>
 <221> misc_feature
 <222> (785)
 <223> y equals c or t

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<400> 26
gggcatgggg cggtcggttc tgctgtgggg agctgcccgc tttctgctgg gaggtctggat 60
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ctacagattc aacggtgatg aggcctatga ccagtgcacc aactaccttc tccaggaagg 240
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1567

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<210> 27
<211> 170
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (89)
<223> Xaa equals any amino acid

<220>
<221> SITE
<222> (132)
<223> Xaa equals any amino acid

<220>
<221> SITE
<222> (138)
<223> Xaa equals any amino acid

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<400> 27
Met Gly Arg Leu Val Leu Leu Trp Gly Ala Ala Val Phe Leu Leu Gly
  1             5             10             15

Gly Trp Met Ala Leu Gly Gln Gly Gly Ala Ala Glu Gly Val Gln Ile
      20             25             30

Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala

```

35 40 45
 Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly
 50 55 60
 Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His
 65 70 75 80
 Thr Ser Gly Cys Leu Leu Asp Ala Xaa Gln Arg Asp Asp Ile Leu Tyr
 85 90 95
 Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp
 100 105 110
 Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Arg
 115 120 125
 Gly Ile Arg Xaa Asp Gly Asp Val Phe Xaa Thr Cys Pro Thr Gly Ile
 130 135 140
 Ser Ser Met Arg Phe Ser Thr Gly Ala Pro Ser Thr Pro Ser Gly Ser
 145 150 155 160
 Pro Asn Arg Lys Ile Pro Ala Thr Ser Pro
 165 170

<210> 28

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer_Bind

<223> Synthetic primer to amplify the cDNA sequence encoding the amino acids Met 1 to Lys 231 including the AUG initiation codon and the naturally associated leader,also contains a BglII site,and Kozak signal

<400> 28

ccgggttagat ctgccatcat ggggcggctg gttctg

36

<210> 29

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer_Bind

<223> Synthetic primer to amplify the cDNA sequence encoding the amino acids Met 1 to Lys 231,also contains a BglII site

<400> 29

ggccggtcta gatttgaca gctttggttt g

31

<210> 30

<211> 4

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any amino acid

<400> 30

Trp Xaa Trp Ser

1

<210> 31

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer_Bind

<223> Synthetic primer to amplify the cDNA sequence encoding the amino acids Met 1 to Lys 231,also contains a XbaI site

<400> 31

ggccggtcta gattatttgg acagcttgg ttg

34

<210> 32

<211> 144

<212> DNA

<213> Artificial Sequence

<220>

<221> Primer_Bind

<223> Synthetic primer to amplify DNA encoding amino acids M1-K231 of SEQ ID NO:2, contains a BglII restriction site.

<400> 32

ccggttagat ctgccatcat gggcggtctg gttctgccgg ttagatctgc catcatgggg 60
cggctggttc tgccggttag atctgccatc atggggcggc tggttctgcc ggtagatct 120
gccatcatgg ggcggctggt tctg 144